REMARKS

A. Regarding the Amendments

The amendments to the specification add the SEQ ID NOs to the Brief Description of the Figures and the Specification. These amendments do not involve new matter and entry is respectfully requested.

CONCLUSION

In summary, for the reasons set forth herein, Applicants submit that the present Response is in compliance with the requirements of 37 CFR 1.121 and respectfully request entry of the amendments set forth herein.

If the Examiner would like to discuss any of the issues raised in the Office Action, Applicant's representative can be reached at (858) 677-1456. Please charge any additional fees, or make any credits, to Deposit Account No. 50-1355.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE FIGURES:

The "Brief Description of the Figures" section has been amended as follows:

At page 4, line 29:

"Figure 1a shows: Amino acid sequence of GCN4-p1 (SEQ ID NO: 4)."

At page 5 line 28 to page 6, line 2:

"Figure 3b shows mobility shift assay of Leu-bZip and Tfl-bZip binding to oligonucleotides containing the AP-1 binding site (5'-GTGGAGATGACTCATCTCCGG-3' (SEQ ID NO: 1), top) the CREB binding site (5'-TGGAGATGACGTCATCTCCT-3' (SEQ ID NO: 2), middle) and the nonspecific sequence (NON, 5'-GATCCCAACACGTGTTGGGATC-3' (SEQ ID NO: 3), bottom), as described in Example 6."

At page 6, lines 4-5:

--Figure 4a shows Amino acid sequence of a leucine-zipper peptide designated A1 (SEQ ID NO: 5), The leucine positions are highlighted in bold.--

IN THE SPECIFICATION:

The following paragraphs have been amended as shown:

At page 16, line 18 to page 17, line 4:
"The amino acid sequence of GCN4-p1 (SEQ ID NO: 4) is shown in Figure 1A. Both the "wild type" (Leu-GCN4-p1) and fluorinated (Tfl-GCN4-p1) forms of the leucine zipper peptide GCN4-p1were synthesized at the Biopolymer Synthesis Center at the California Institute of Technology (Pasadena, CA 91125). Automated, stepwise solid-phase synthesis was performed in an ABI 433A synthesizer employing Fmoc chemistry. To prepare the fluorinated peptide (Tfl-GCN4-p1), *N*-Fmoc-5, 5, 5-trifluoro-L-leucine prepared as described

in Example 1was used as an equimolar mixture of the 2S,4S- and the 2S,4R- isomers, and incorporated into the peptide with extended coupling cycles. After chain assembly was complete, the peptide was deprotected and removed from the resin support with trifluoroacetic acid in the presence of 1,2-ethanedithiol, thioanisole and water. Peptides were precipitated into cold methyl t-butyl ether and isolated by centrifugation. Peptide products were purified by preparative C_{18} reverse phase HPLC using a non-linear gradient of 0-80% elution solution (0.1%TFA/60% acetonitrile/ 40% H_2O in 120 min. Neither Leu-GCN4-p1 nor Tfl-GcN4-p1 is acetylated at the N-terminus; hence the thermal melting temperature of Lau-GCN4-p1 is lower than that reported for acetylated GCN4-p1. After HPLC purification, the molar mass of Tfl-GCN4-p1 was confirmed to be 4213 Da, 216 mass units higher than that of Leu-GCN4-p1."

Page 17, lines 11-15:
"Analog Incorporation Assay. The expression vector pQE-A1, which contains the coding sequences for the protein A1 (SEQ ID NO: 5) (Figure 4A) was obtained from US Army Natick RD&E Center (Natick, MA). The *E. coli* leucine auxotroph SG13009 was obtained from Qiagen (Chatsworth, CA) and transformed with plasmids pREP4 and pQE-A1, to yield the expression host LAE-A1."

Page 28, lines 14 - 23:
"The A1 protein (SEQ ID NO: 5) (Figure 4A) forms dimeric coiled coils in aqueous solution. It has been previously used as an element of artificial multidomain proteins that form reversible hydrogels under conditions of controlled pH and temperature(Petka, W.A.; Harden, J.L.; McGrath, K.P.; Wirtz, D. Tirrell, D.A. *Science* 1998, *281*, 389-392). The A1 protein contains eight leucine resudues, of which six are distributed at the ***d*** positions of the six heptad repeats. By using a leucine auxotrophic strain of *E. coli*, trifluoroleucine-substituted A1 was prepared at levels of fluorination that ranged from 17% to 92%. The thermal and chemical stabilities of the fluorinated proteins were significantly elevated compared to those

of the wide type A1 protein. Hfl does not support measurable protein synthesis in *E. coli* under the conditions examined in this example."